What is claimed is:

1. An isolated polynucleotide from coryneform bacteria, comprising an elongated sequence coding for 1-phosphofructokinase and/or 6-phosphofructokinase, wherein said sequence is elongated in front of the start codon and behind the stop codon of the gene, in each instance by up to about 700 base-pairs.

2. The isolated polynucleotide according to Claim 1, wherein the elongated amino-acid sequence is represented by SEQ ID NO: 3 for the 1-phosphofructokinase gene and by SEQ ID NO: 1 for the 6-phosphofructokinase gene and the elongation in comparison with the sequence known from the state of the art consisting in SEQ ID NO: 3 of base-pairs 1 to 508 and 1684 to 2234 and in SEQ ID NO: 1 of base-pairs 1 to 531 and 1621 to 2160.

3. A process for the fermentative preparation of L-amino acids in coryneform bacteria, comprising:

   a) fermenting the coryneform bacteria producing the desired L-amino acid, in which at least the gene coding for 6-phosphofructokinase and/or the gene coding for 1-phosphofructokinase are/is attenuated.

4. The method according to claim 3, further comprising:

   b) enriching the produced L-amino acids in the medium or in the cells of the bacteria.

5. The method according to claim 4, further comprising:

   c) isolating the L-amino acid.

6. The method according to claim 5, wherein the medium includes a fermentation broth and constituents of the

fermentation broth remain in the end product in some proportion of their original quantity.

7. The method according to claim 5, wherein constituents of a biomass of the cells remain in the end product in some proportion of their original quantity.

8. The method according to claim 3, wherein the L-amino acids are L-lysine.

9. The method according to Claim 3, wherein coryneform bacteria are employed in which the attenuation is achieved by using polynucleotide sequences that are elongated in front of the start codon and behind the stop codon of the respective gene by, in each instance, 300 to 800 base-pairs.

10. The method according to Claim 9, wherein coryneform bacteria are employed in which the attenuation is achieved by using polynucleotide sequences that are elongated in front of the start codon and behind the stop codon of the gene, in each instance by about 700 base-pairs, the elongated nucleotide sequences being represented in SEQ ID NO: 3 for the 1-phosphofructokinase gene and in SEQ ID NO: 1 for the 6-phosphofructokinase gene and the elongations in SEQ ID NO: 3 in comparison with the sequence known from the state of the art consisting of base-pairs 1 to 508 and 1684 to 2234 and in SEQ ID NO: 1 in comparison with the sequence known from the state of the art consisting of base-pairs 1 to 531 and 1621 to 2160.

11. The method according to Claim 3, wherein the bacteria comprise additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced

12. The method according to Claim 3, wherein bacteria are employed in which the metabolic pathways that diminish

the formation of the desired L-amino acid are at least partially switched off.

13. The method according to Claim 3, wherein the expression of the polynucleotide(s) that codes/code for 6-phosphofructokinase and/or for 1-phosphofructokinase is diminished.

14. The method according to Claim 3, wherein the catalytic properties of the polypeptide(s) (enzyme protein(s)) for which the polynucleotide(s) from SEQ ID NO. 1 and SEQ ID No. 3 codes/code are reduced.

15. The method according to claim 3, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced; wherein the one or more genes is/are selected from the group consisting of:

the gene lysC coding for a feedback-resistant aspartate kinase,

the gene dapA coding for dihydrodipicolinate synthase,

the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,

the gene pyc coding for pyruvate carboxylase,

the gene mqo coding for malate:quinone oxidoreductase,

the gene zwf coding for glucose-6-phosphate dehydrogenase,

simultaneously the gene lysE coding for lysine export,

the gene zwa1 coding for the zwa1 protein,

the gene tpi coding for triosephosphate isomerase, and

the gene pgk coding for 3-phosphoglycerate kinase.

16. The method according to claim 3, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the one or more genes is/are selected from the group consisting of:

the pck gene coding for phosphoenolpyruvate carboxykinase,

the pgi gene coding for glucose-6-phosphate isomerase,

the gene poxB coding for pyruvate oxidase,

the gene fda coding for fructose bisphosphate aldolase, and

the gene zwa2 coding for the zwa2 protein.

17. The method according to claim 3, wherein micro-organisms of the species Corynebacterium glutamicum are employed.

18. A coryneform bacterium in which at least the gene coding for 6-phosphofructokinase and/or the gene coding for 1-phosphofructokinase are/is present in attenuated form.

19. An escherichia coli strain DH5alphamcr/pXK99EmobpfkB (= DH5αmcr/ pXK99EmobpfkB), deposited as DSM 14741.